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<130> 00-108

<151> 2000-11-28

<151> 2001-02-07

<160> 50

<170> FastSEQ for Windows Version 3.0

 $\langle 210 \rangle$ 1

<211> 1476

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)...(1473)

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg 96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
20 25 30

ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc 144

Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
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aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
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Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu	
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cta	tgt	tct	atg	atg	tgc	ctg	aag	aaa	cag	gac	ctg	tac	aac	aag	ttc	288
Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe	
				85				90						95		
aag	gga	cgc	gtg	cgg	acg	gtt	tct	ccc	agc	tcc	aag	tcc	ccc	tgg	gtg	336
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val	
			100				105						110			
gag	tcc	gaa	tac	ctg	gat	tac	ctt	ttt	gaa	gtg	gag	ccg	gcc	cca	cct	384
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro	
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Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
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Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Phe	Leu	Lys	Tyr	Glu	Val	
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Ala	Phe	Trp	Gly	Gly	Gly	Ala	Gly	Thr	Lys	Thr	Leu	Phe	Pro	Val	Thr	
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ccc	cat	ggc	cag	cca	gtc	cag	atc	act	ctc	cag	cca	gct	gcc	agc	gaa	576
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
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cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	624
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
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gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu 225 230 235 240	720
gta att gcc gca ggg ggt gtg atc tgg aag acc ctc atg ggg aac ccc Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro 245 250 255	768
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Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
20 25 30
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
35 40 45

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Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
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Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
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Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro
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Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Glu	Leu	Thr	Arg	Gly
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Trp	Lys	Lys	Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp
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Leu	Gly	Gln	Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val
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Asp	Ser	Gly	Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser
			340					345					350		
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Gln Gly Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu
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 Phe Ser Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu
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 Ser Ser Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val
 420 425 430
 Pro Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu
 435 440 445
 Ser Ser Pro Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp
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<212> DNA

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ytnacntggy tncnnggnyt nggnaayccn cargaygt na cntayttygt ngcntaycar	180
wsnwsnccna cmgmngmng ntggmgngar gtngargart gygcnggnac naargarytn	240
ytnygywsna tgatgtgyt naaraarcar gayytnytna ayaarttyaa rggnmngntn	300
mgnacngtnw snccnwsnws naarwsnccn tgggtngarw sngartayyt ngaytayytn	360
ttygargtng arcngcnc nccngtnytn gtynytnacn araccngarga rathytnwsn	420
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gcnttytggg gngngngngc nggnacnaar acnytnntyc cngtnacncc ncayggncar	540
ccngtnccara thacnytnca rccngcngcn wsngarcayc aytgyytnws ngcnmgncn	600
athtayacnt tywsngtncc naartaywsn aarttywsna arccnacntg yttyytnytn	660
gargtnccng argcnaaytg ggcnttyytn gtynytnccn snytnytnat hytnytnytn	720
gtathgcn gngngngngt nathtggaar acnytnatgg gnaaycctg gttcarmgn	780
gcnaaratgc cmngngcny ngarytnacn mgngngntm gncnacncc nmngntnmgn	840
gcncngcna cncarcac nmgntggaar aargayytn cngargayga rgargargar	900

gaygargarg ayacngarga yggngtnwsn ttycarccnt ayathgarcc nccnwsntty 960
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 Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr Arg Arg Arg Trp
 35 40 45
 Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu Leu Cys Ser Met
 50 55 60
 Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe Lys Gly Arg Val
 65 70 75 80
 Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val Glu Ser Glu Tyr
 85 90 95
 Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro Val Leu Val Leu
 100 105 110
 Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr Tyr Gln Leu Pro
 115 120 125
 Pro Cys Met Pro Pro Leu Phe Leu Lys Tyr Glu Val Ala Phe Trp Gly
 130 135 140
 Gly Gly Ala Gly Thr Lys Thr Leu Phe Pro Val Thr Pro His Gly Gln
 145 150 155 160
 Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu His His Cys Leu
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<223> Oligonucleotide primer ZC17574

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<213> Artificial Sequence

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Glu Tyr Met Pro Met Glu

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<213> Artificial Sequence

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<223> FLAG peptide tag

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Asp Tyr Lys Asp Asp Asp Lys

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<210> 13

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<213> Homo sapiens

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accctgagg	tcacatgctg	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
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aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
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ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc	144
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser	
35 40 45	
ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc	192
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser	
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Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr	
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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys	
85 90 95	
aaa gtt gag ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc	336
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys	
100 105 110	
cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca	384
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro	
115 120 125	
aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc	432
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys	
130 135 140	
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Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp	
145 150 155 160	
tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag	528
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu	
165 170 175	
gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg	576
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu	
180 185 190	

cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac 624
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205

aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg 672
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220

cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag 720
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240

ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat 768
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255

ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac 816
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270

aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc 864
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285

ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac 912
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 290 295 300

gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg 960
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
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 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

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<211> 330

<212> PRT

<213> Homo sapiens

099599 1280

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Phe	Pro	Glu 35	Pro	Val	Thr	Val	Ser 40	Trp	Asn	Ser	Gly	Ala 45	Leu	Thr	Ser
Gly	Val	His 50	Thr	Phe	Pro	Ala 55	Val	Leu	Gln	Ser	Ser	Gly 60	Leu	Tyr	Ser
Leu 65	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr 80
Tyr	Ile	Cys	Asn 85	Val	Asn	His	Lys	Pro	Ser 90	Asn	Thr	Lys	Val	Asp 95	Lys
Lys	Val	Glu 100	Pro	Lys	Ser	Cys	Asp	Lys 105	Thr	His	Thr	Cys	Pro	Pro	Cys
Pro	Ala	Pro 115	Glu	Leu	Leu	Gly	Gly 120	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
Lys	Pro	Lys 130	Asp	Thr	Leu	Met	Ile 135	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
Val 145	Val	Val	Asp	Val	Ser	His	Glu 150	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp 160
Tyr	Val	Asp	Gly 165	Val	Glu	Val	His	Asn 170	Ala	Lys	Thr	Lys	Pro	Arg	Glu
Glu	Gln	Tyr	Asn 180	Ser	Thr	Tyr	Arg	Val 185	Val	Ser	Val	Leu	Thr	Val	Leu
His	Gln	Asp 195	Trp	Leu	Asn	Gly	Lys 200	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
Lys	Ala	Leu 210	Pro	Ala	Pro	Ile 215	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
Gln 225	Pro	Arg	Glu	Pro	Gln	Val	Tyr 230	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
Leu	Thr	Lys	Asn 245	Gln	Val	Ser	Leu	Thr 250	Cys	Leu	Val	Lys	Gly	Phe	Tyr
Pro	Ser	Asp	Ile 260	Ala	Val	Glu	Trp 265	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
Asn	Tyr	Lys 275	Thr	Thr	Pro	Pro	Val 280	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
Leu	Tyr	Ser 290	Lys	Leu	Thr	Val	Asp 295	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
Val 305	Phe	Ser	Cys	Ser	Val	Met	His 310	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
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<222> (1)...(1563)

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Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu	
			20					25					30			
ctc	tcc	cag	aac	ttc	agc	gtg	tac	ctg	aca	tgg	ctc	cca	ggg	ctt	ggc	144
Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly	
		35					40					45				
aac	ccc	cag	gat	gtg	acc	tat	ttt	gtg	gcc	tat	cag	agc	tct	ccc	acc	192
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr	
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cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	240
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
65 70 75 80	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	288
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
85 90 95	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	336
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
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gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	384
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
115 120 125	
gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg	432
Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr	
130 135 140	
tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag gtg	480
Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val	
145 150 155 160	
gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc act	528
Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr	
165 170 175	
ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc gaa	576
Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu	
180 185 190	
cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg aaa	624
His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys	
195 200 205	
tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca gaa	672
Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu	
210 215 220	
gcc aac tgg gct ttc ctg gtg ctg cca tcg ctt ctg ata ctg ctg tta	720

Ala	Asn	Trp	Ala	Phe	Leu	Val	Leu	Pro	Ser	Leu	Leu	Ile	Leu	Leu	Leu	
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gta	att	gcc	gca	ggg	ggt	gtg	atc	tgg	aag	acc	ctc	atg	ggg	aac	ccc	768
Val	Ile	Ala	Ala	Gly	Gly	Val	Ile	Trp	Lys	Thr	Leu	Met	Gly	Asn	Pro	
				245					250					255		
tgg	ttt	cag	cgg	gca	aag	atg	cca	cgg	gcc	ctg	gac	ttt	tct	gga	cac	816
Trp	Phe	Gln	Arg	Ala	Lys	Met	Pro	Arg	Ala	Leu	Asp	Phe	Ser	Gly	His	
			260					265					270			
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Thr	His	Pro	Val	Ala	Thr	Phe	Gln	Pro	Ser	Arg	Pro	Glu	Ser	Val	Asn	
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gac	ttg	ttc	ctc	tgt	ccc	caa	aag	gaa	ctg	acc	aga	ggg	gtc	agg	ccg	912
Asp	Leu	Phe	Leu	Cys	Pro	Gln	Lys	Glu	Leu	Thr	Arg	Gly	Val	Arg	Pro	
	290					295					300					
acg	cct	cga	gtc	agg	gcc	cca	gcc	acc	caa	cag	aca	aga	tgg	aag	aag	960
Thr	Pro	Arg	Val	Arg	Ala	Pro	Ala	Thr	Gln	Gln	Thr	Arg	Trp	Lys	Lys	
305					310					315					320	
gac	ctt	gca	gag	gac	gaa	gag	gag	gag	gat	gag	gag	gac	aca	gaa	gat	1008
Asp	Leu	Ala	Glu	Asp	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Asp	Thr	Glu	Asp	
				325					330					335		
ggc	gtc	agc	ttc	cag	ccc	tac	att	gaa	cca	cct	tct	ttc	ctg	ggg	caa	1056
Gly	Val	Ser	Phe	Gln	Pro	Tyr	Ile	Glu	Pro	Pro	Ser	Phe	Leu	Gly	Gln	
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gag	cac	cag	gct	cca	ggg	cac	tcg	gag	gct	ggt	ggg	gtg	gac	tca	ggg	1104
Glu	His	Gln	Ala	Pro	Gly	His	Ser	Glu	Ala	Gly	Gly	Val	Asp	Ser	Gly	
		355					360					365				
agg	ccc	agg	gct	cct	ctg	gtc	cca	agc	gaa	ggc	tcc	tct	gct	tgg	gat	1152
Arg	Pro	Arg	Ala	Pro	Leu	Val	Pro	Ser	Glu	Gly	Ser	Ser	Ala	Trp	Asp	
	370					375					380					
tct	tca	gac	aga	agc	tgg	gcc	agc	act	gtg	gac	tcc	tcc	tgg	gac	agg	1200
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<212> PRT
<213> Homo sapiens
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 35 40 45
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140
 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
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 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
 165 170 175
 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
 180 185 190
 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
 195 200 205
 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Glu
 210 215 220
 Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu Ile Leu Leu Leu
 225 230 235 240
 Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu Met Gly Asn Pro
 245 250 255
 Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp Phe Ser Gly His
 260 265 270
 Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg Pro Glu Ser Val Asn
 275 280 285
 Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr Arg Gly Val Arg Pro
 290 295 300
 Thr Pro Arg Val Arg Ala Pro Ala Thr Gln Gln Thr Arg Trp Lys Lys
 305 310 315 320
 Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Thr Glu Asp
 325 330 335
 Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly Gln
 340 345 350
 Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser Gly
 355 360 365

Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp Asp
 370 375 380
 Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp Arg
 385 390 395 400
 Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly Pro
 405 410 415
 Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser Lys
 420 425 430
 Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser Trp
 435 440 445
 Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Asn Leu Val Pro Gly Gly
 450 455 460
 Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser Ser Pro
 465 470 475 480
 Glu Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser Asp Ala
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<213> Homo sapiens

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gcc gct cca ggg agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	96
Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
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ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	144
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
35 40 45	

aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc 192
 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
 50 55 60

cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg 240
 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
 65 70 75 80

cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc 288
 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
 85 90 95

aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg 336
 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
 100 105 110

gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct 384
 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
 115 120 125

gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc acg 432
 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
 130 135 140

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 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
 145 150 155 160

gca ttc tgg aag gag ggg gcc gga aac aag gtg gga agc tcc ttt cct 528
 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Val Gly Ser Ser Phe Pro
 165 170 175

gcc ccc agg cta ggc ccg ctc ctc cac ccc ttc tta ctc agg ttc ttc 576
 Ala Pro Arg Leu Gly Pro Leu Leu His Pro Phe Leu Leu Arg Phe Phe
 180 185 190

tca ccc tcc cag cct gct cct gca ccc ctc ctc cag gaa gtc ttc cct 624
 Ser Pro Ser Gln Pro Ala Pro Ala Pro Leu Leu Gln Glu Val Phe Pro
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674

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<221> CDS

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Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgt aga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg ctg	144
Phe Arg Arg Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu	
35 40 45	
ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt ggc	192
Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly	
50 55 60	
aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc acc	240
Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr	
65 70 75 80	
cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag ctg	288
Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu	
85 90 95	
cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag ttc	336
Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe	
100 105 110	
aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg gtg	384
Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val	
115 120 125	
gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca cct	432
Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro	
130 135 140	

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Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr	
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Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val	
				165					170						175	
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Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr	
			180					185					190			
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Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu	
		195					200					205				
cac	cac	tgc	ctc	agt	gcc	aga	acc	atc	tac	acg	ttc	agt	gtc	ccg	aaa	672
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys	
	210					215					220					
tac	agc	aag	ttc	tct	aag	ccc	acc	tgc	ttc	ttg	ctg	gag	gtc	cca	gaa	720
Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu	
225					230					235					240	
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Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
				245					250					255		
gca	cct	gaa	gcc	gag	ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	816
Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
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Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
		275					280					285				
gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	912
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
	290					295					300					
gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	960
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
305					310					315					320	

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 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 325 330 335

cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa 1056
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350

gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc aaa ggg cag 1104
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 355 360 365

ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg 1152
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 370 375 380

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 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400

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 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415

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 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 420 425 430

tac agc aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc 1344
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 435 440 445

ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag 1392
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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<212> PRT

<213> Artificial Sequence

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Phe	Arg	Arg	Ser	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
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	50					55					60				
Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
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Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
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Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
			100					105					110		
Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
	115					120						125			
Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
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Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
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Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
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Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
			180					185					190		
Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Ser	Glu
	195					200						205			
His	His	Cys	Leu	Ser	Ala	Arg	Thr	Ile	Tyr	Thr	Phe	Ser	Val	Pro	Lys
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Tyr	Ser	Lys	Phe	Ser	Lys	Pro	Thr	Cys	Phe	Leu	Leu	Glu	Val	Pro	Glu
225					230					235				240	
Ala	Asn	Trp	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
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Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	260						265						270		
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
	275					280						285			
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr
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0995555 1122004

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 305 310 315 320
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
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 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 340 345 350
 Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 355 360 365
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
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 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 385 390 395 400
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 405 410 415
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
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 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
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22

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NO:19

<221> misc_feature

<222> (1)...(1560)

<223> n = A,T,C or G

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ytnacntggy tncnggnytn nggnaayccn cargaygt na cntayttygt ngcntaycar	180
wsnwsnccna cnmgnmgnmg ntggmngar gtngargart gygcnggnac naargarytn	240
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mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480
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ccngtncara	thacnytnca	rccngcngcn	wsngarcayc	aytggytnws	ngcnmgnacn	600
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gargtnccng	argcnaaytg	ggcnttyytn	gtnytnccnw	snytnytnat	hytnytnytn	720
gtathgcng	cngggnggt	nathtggaar	acnytnatgg	gnaayccntg	gttycarmgn	780
gcnaaratgc	cnmgngcny	ngayttywsn	ggncayacnc	ayccngtngc	nacnttycar	840
ccnwsnmgnc	cngarwsngt	naaygayytn	ttyytnntgy	cncaraarga	rytnacnmgn	900
ggngtnmgnc	cnacnccnmg	ngtnmgngcn	ccngcnacnc	arcaracnmg	ntggaaraar	960
gayytnngcng	argaygarga	rgargargay	gargargaya	cngargaygg	ngtnwsntty	1020
carcentaya	thgarccncc	nwsnttyytn	ggncargarc	aycargcncc	nggncaywsn	1080
gargcnggng	ngtngayws	nggnmgncn	mgngcnccny	tngtnccnws	ngarggnwsn	1140
wsngcntggg	aywsnwsnga	ymgnwsntgg	gcnwsnacng	tngaywsnws	ntgggaymgn	1200
gcnggnwsnw	snggntayyt	ngcngaraar	ggncnccngc	arggncnccg	nggngaygg	1260
caycargarw	snytnccncc	nccngartty	wsnaargayw	snggnttyyt	ngargarytn	1320
ccngargaya	ayytnwsnws	ntgggcnacn	tggggnacny	tnccnccnga	rccnaayytn	1380
gtncnccngg	gnccnccngt	nwsnytnear	acnytnacnt	tytgytgga	rwsnwsnccn	1440
gargargarg	argargcnmg	ngarwsngar	athgargayw	sngaygcngg	nwsntggggg	1500
gcngarwsna	cncarmgnac	ngargaymgn	ggnmgnacny	tnggncayta	yatggcnmgn	1560

<210> 29

<211> 633

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of SEQ ID NO:21

<221> misc_feature

<222> (1)...(633)

<223> n = A,T,C or G

<400> 29

atggcnggnc	cngarmgntg	gggncnnytn	ytnytnntgy	tnytneargc	ngcncnccng	60
mgncnccmgy	tnccnccncc	ncaraaygt	acnytnytnw	sncaraaytt	ywsngntay	120
ytnacntggy	tnccnccngt	nggnaayccn	cargaygt	cntaytygt	ngcntaycar	180
wsnwsnccna	cnmgnmgnmg	ntggmgngar	gtngargart	gygcnggnac	naargarytn	240
ytnytnytnw	tgatgtgyyt	naaraarcar	gayytnntay	ayaarttyaa	rggnmgngtn	300
mgnacngtnw	sncnwsnws	naarwsnccn	tgggtngarw	sngartayyt	ngaytayytn	360
ttygargtn	arccngcncc	nccngtnytn	gtnytnacnc	aracngarga	rathytnwsn	420
gcnaaygcna	cntaycaryt	nccncntgy	atgccnccny	tngayytnaa	rtaygargtn	480

gcnttytgga argarggngc nggnaayaar gtnggnwsnw snattyccngc nccnmgnytn 540
 ggncnnytny tncayccntt yytnytnmgn ttyttywsnc cnwsncarcc ngcncngcn 600
 ccnytnytn c argargtntt yccngtncay wsn 633

<210> 30

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39204

<400> 30

tcaccacgcg aattcggtag cgctggttcc gcgtggatcc aggccccgtc tggccccctcc 60
 ccag 64

<210> 31

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide Primer ZC39205

<400> 31

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ccagttggct tctgggacct 60
 ccag 64

<210> 32

<211> 1922

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP-human zcytoR19 fusion protein polynucleotide
 sequence

<221> CDS

<222> (123)...(1922)

<400> 32

ttgacaatta atcatcggct cgtataatgt gtggaattgt gagcggataa caatttcaca 60
 caggaaacag ccagtccgtt taggtgtttt cagagcact tcaccaacaa ggaccataga 120

tt atg aaa act gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp 1 5 10 15	167
aaa ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat Lys Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp 20 25 30	215
acc gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa Thr Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys 35 40 45	263
ttc cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg Phe Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp 50 55 60	311
gca cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa Ala His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu 65 70 75	359
atc acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg Ile Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp 80 85 90 95	407
gat gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt Asp Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val 100 105 110	455
gaa gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca Glu Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro 115 120 125	503
aaa acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa Lys Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys 130 135 140	551
ggt aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg Gly Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp 145 150 155	599
ccg ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc Pro Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly 160 165 170 175	647

aag tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg	695
Lys Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala	
180 185 190	
ggt ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca	743
Gly Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala	
195 200 205	
gac acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca	791
Asp Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr	
210 215 220	
gcg atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc	839
Ala Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser	
225 230 235	
aaa gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca	887
Lys Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro	
240 245 250 255	
tcc aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt	935
Ser Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser	
260 265 270	
ccg aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act	983
Pro Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr	
275 280 285	
gat gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta	1031
Asp Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val	
290 295 300	
gcg ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc	1079
Ala Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala	
305 310 315	
gcc acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg	1127
Ala Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro	
320 325 330 335	
cag atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc	1175

Gln Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala	
340 345 350	
gcc agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act	1223
Ala Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr	
355 360 365	
aat tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg	1271
Asn Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu	
370 375 380	
gtt ccg cgt gga tcc agg ccc cgt ctg gcc cct ccc cag aat gtg acg	1319
Val Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr	
385 390 395	
ctg ctc tcc cag aac ttc agc gtg tac ctg aca tgg ctc cca ggg ctt	1367
Leu Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu	
400 405 410 415	
ggc aac ccc cag gat gtg acc tat ttt gtg gcc tat cag agc tct ccc	1415
Gly Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro	
420 425 430	
acc cgt aga cgg tgg cgc gaa gtg gaa gag tgt gcg gga acc aag gag	1463
Thr Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu	
435 440 445	
ctg cta tgt tct atg atg tgc ctg aag aaa cag gac ctg tac aac aag	1511
Leu Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys	
450 455 460	
ttc aag gga cgc gtg cgg acg gtt tct ccc agc tcc aag tcc ccc tgg	1559
Phe Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp	
465 470 475	
gtg gag tcc gaa tac ctg gat tac ctt ttt gaa gtg gag ccg gcc cca	1607
Val Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro	
480 485 490 495	
cct gtc ctg gtg ctc acc cag acg gag gag atc ctg agt gcc aat gcc	1655
Pro Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala	
500 505 510	

acg tac cag ctg ccc ccc tgc atg ccc cca ctg gat ctg aag tat gag 1703
 Thr Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu
 515 520 525

gtg gca ttc tgg aag gag ggg gcc gga aac aag acc cta ttt cca gtc 1751
 Val Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val
 530 535 540

act ccc cat ggc cag cca gtc cag atc act ctc cag cca gct gcc agc 1799
 Thr Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser
 545 550 555

gaa cac cac tgc ctc agt gcc aga acc atc tac acg ttc agt gtc ccg 1847
 Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro
 560 565 570 575

aaa tac agc aag ttc tct aag ccc acc tgc ttc ttg ctg gag gtc cca 1895
 Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro
 580 585 590

gaa gcc aac tgg tgt ttt ggc gga tga 1922
 Glu Ala Asn Trp Cys Phe Gly Gly *
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<210> 33

<211> 599

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-human zcytoR19 fusion protein polypeptide
 sequence

<400> 33

Met Lys Thr Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60

00955660

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
 385 390 395 400

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<210> 34
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(20)
<223> Xaa = Any Amino Acid
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<400> 34
Ser Arg Pro Arg Leu Ala Pro Pro Gln Xaa Val Thr Leu Leu Ser Gln
1 5 10 15
Asn Phe Ser Val
20

<210> 35
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC40285

<400> 35
 gccccagcca cccaacagac aaga 24

<210> 36
 <211> 24
 <212> DNA
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<220>
 <223> Oligonucleotide primer ZC40286

<400> 36
 ccaggtggcc caggaggaga gggt 24

<210> 37
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC39128

<400> 37
 ggcatggaag ataatgaaag gaaa 24

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC39129

<400> 38
 gccgtcactc ccaactgggg atgt 24

<211> 25

<213> Artificial Sequence

<223> Oligonucleotide primer ZC40784

ggatagtggt ttgagtttct gtgga

25

<211> 25

<213> Artificial Sequence

<223> Oligonucleotide primer ZC40785

accaggagtt caaggttaac cttgg

25

<211> 24

<213> Artificial Sequence

<223> Oligonucleotide primer ZC40786

gggaattcct gcagaaactc agta

24

<211> 24

<213> Artificial Sequence

<223> Oligonucleotide primer ZC40787

<400> 42

cccttcctgc tcctttgact gcgt

24

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39408

<400> 43

gcccagctgc atcttcctag aggc

24

<210> 44

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39409

<400> 44

gggcattgcc aggacagctc ttttg

25

<210> 45

<211> 121

<212> DNA

<213> Artificial Sequence

<220>

<223> forward zcytor19 knockout oligonucleotide

<400> 45

cacctgccgc ccaggggcct tgcggcgggc ggcggggacc ccagggaccg aaggccatag
cggccggccc ctaggatccg aattctagaa gctttgtgtc tcaaaatctc tgatgttaca
t

60

120

121

<210> 46

<211> 125

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse zcytor19 knockout oligonucleotide

<400> 46

ggctggtccc ctgcaagagt agcaagcgct tcttcagcat ccggacttac ggcctcgctg	60
gccggcgcg ctaggaattc tctagaggat ccaagctttt agaaaaactc atcgagcatc	120
aaatg	125

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38481

<400> 47

cctccttcca gaatgccacc tc	22
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<210> 48

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38626

<400> 48

ctgctatggt ctatgatgtg cctga	25
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<210> 49

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38706

<400> 49

ggaagataat gaaaggaaac cc	22
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<210> 50

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38711

<400> 50

tatgaggagt cccctgtgct g

21

p.038711 "ZC38711"